Proc. Assoc. Advmt. Anim. Breed. Genet. 26: 50-53

GENETIC ANALYSIS OF SENSOR-BASED ACTIVITY IN AUSTRALIAN MERINO SHEEP

H. Keshavarzi[1], E. Dehnavi[2], J. McNally[1], J.L. Smith[1] and S. Schmoelzl[1]

[1] CSIRO Agriculture and Food, Armidale, NSW, 2350 Australia
[2] Animal Genetics Breeding Unit*, University of New England, Armidale, NSW 2351
Australia

SUMMARY

The use of on-animal sensor data enables continuous monitoring, providing valuable behavioural observations with the potential to be used for assessing an individual's health and productivity. This study aimed to estimate the genetic parameters of sheep general activity, measured as vector magnitude, which represents the overall magnitude of the movement to provide an objective activity level measurement. Activity records of 1,149 Merino ewes were collected with ActiGraph™ wGT3X-BT® devices over a period of 17 days (after editing 10 non-continuous days used in the analysis). Single trait estimates (STE) were initially considered for this analysis; however, random regression (RR) was also checked, given the patterns observed on raw records over time and days. The STE of heritability (h^2) and repeatability (Rep) in the whole dataset were 0.19 ± 0.06 and 0.56 ± 0.08, respectively. Across 10 days, single estimates of h^2 ranged from 0.15 ± 0.06 to 0.25 ± 0.08 and Rep from 0.45 ± 0.08 to 0.66 ± 0.08, while RR models resulted in lower h^2 (0.11 to 0.23) and Rep (0.22 to 0.34) over these days. Genetic correlations between days (up to day 16) and times (2 hours) were high, which did not indicate the potential of random effects of time and day in genetic parameters for sheep activity. These estimated parameters can be considered for future welfare-related breeding programs, and the amount of repeatability can guide the development of an effective measurement protocol.

INTRODUCTION

Recent research emphasises using sensor technologies to monitor animal better and measure the animals' behaviour, health, and production traits in commercial systems (Almasi *et al.* 2023; Brito *et al.* 2020). Accelerometer data can be used to classify behaviours (Wang *et al*. 2023) or quantified as activity levels (Marchesini *et al*. 2018; Hu *et al*. 2024). These novel traits may be heritable and, once validated, could be incorporated into breeding programs by providing more detailed and consistent information which enables superior genetic comparisons over time (Morris *et al.* 2012) or establishing correlations between behavioural and health traits and improve animal behaviour and welfare. Therefore, this study aimed to estimate the genetic parameters of sheep activity, measured as vector magnitude count (VMC) using linear, repeated measurement and random regression models.

MATERIALS AND METHODS

In this study, the activity data of two contemporary groups of Merino ewes born in 2017 (n=607, recorded in Dec 2022 - Jan 2023) and 2018 (n =542, recorded in Dec 2023 - Jan 2024) were used. The sheep were F1 ewes from the New England Merino Lifetime Productivity flock (MLP), managed by CSIRO at the FD McMaster Laboratory, Chiswick, Uralla, NSW, Australia (Ramsay *et al.* 2019). All experimental procedures conducted on animals were approved by the CSIRO Armidale Animal Ethics Committee (Animal Research Authority no. 21/24 and 22/20).

---

[*] A joint venture of NSW Department of Primary Industries and Regional Development and the University of New England

ActiGraph™ wGT3X-BT® devices (Actigraph LLC, Pensacola, FL, USA) were used to collect sheep activity data continuously at 30 Hz. In its default setting, the 3-axis accelerometer within the device measures accelerations for each axis (X, Y, Z) in G value, estimating VMC as:

$$\text{VMC}= \sqrt{axis\text{x}^2 + axis\text{y}^2 + axis\text{z}^2}.$$

For each experiment, the complete data was available for 17 days. On day one, devices were attached to each sheep's neck using a collar. Raw data was downloaded using ActiLife software, which filtered noise and provided summary outputs as hourly epochs. Outliers and VMC less than 100 were removed from the dataset using a histogram or boxplots for values outside the limit at each timepoint and overall. The days when the animal moved between paddocks or through yards were excluded. To ensure data consistency and reduce number of analyses, only days with records from both deployments (in total 10 non-consecutive days) were used for further analysis. From 24-hour records, 4 one-hour time blocks in the afternoon between 1500 and 1900 h were selected for analysis, based on inter-animal variability during this period, combined with an absence of disruptive events such as moving animals between paddocks (in total times=4, day=10, and daytime=40 records per animal). Variations in activity between animals and over time were expected. However, heterogeneity across contemporary groups was addressed with the method described by Brown *et al.* (2005). In total, 45,641 records from 824 fully pedigreed ewes, representing 28 sires were used.

Statistical analysis. A univariate animal model for repeated measures was fitted using ASReml (Gilmour *et al.* 2009) to estimate heritability (h^2) and repeatability (Rep) of activity across the dataset (single estimates using repeated measurement model (RMM)) and intervals for each time (n=4), day (n=10), and daytime (n=40; although there was not any evidence of autocorrelation in this study, it might be a limitation) to assess the necessity of running RR. Given the unknown pattern of this trait across time, day, and daytime, an RR model with polynomial orders (1 to 6) was also applied to activity across day, time and the interaction of day and time. Models were compared using the likelihood ratio test (LRT), Akaike Information Criterion (AIC), and Bayesian Information Criterion (BIC).

Fixed effects included contemporary groups while day, time, and day-time interaction were fitted separately as repeated measurements. Bodyweight (kg) at 4yo, rainfall (mm), temperature humidity index, wind speed (km/h), and solar radiation (W/m^2) were considered as covariates when time and/or day were fitted as repeated measurements in the model. Random effects comprised genetic and permanent environment effects, with genetic group effects assessed. The covariance function was estimated in RR models using $\hat{G} = \Phi K \Phi'$, where $\hat{G}$ is the genetic covariance matrix for breeding values, Φ is the matrix of orthogonal polynomials, and K is the genetic variance coefficients matrix.

RESULTS AND DISCUSSION

The results showed all covariates and fixed factors were significant ($P < 0.001$) except rainfall information. Animal weight and weather conditions significantly influenced animal activity. Genetic groups (assigned by Sheep Genetics) had no significant effect and were excluded.

A single estimate of h^2 and Rep was obtained by fitting daytime as a repeated measure, with h^2 at 0.19 ± 0.06 and Rep at 0.56 ± 0.08 for all days and times in the dataset. Heritability and Rep values varied (with a pattern) across different times (Figure 1a), days (Figure 1d), and daytimes (Figure 1g; Rep estimates were not computed as they were not repeated) ranging from low to moderate.

Polynomial regression was fitted to the fixed effect of time, day and daytime to find the best order in the raw records. The best fit for the records was achieved by using regression models with polynomial orders of 2 for time and 6 for day (Figure 1c, and f, respectively), resulting in R^2 values close to 1 (Figures 1b and e, respectively). Fitting RR with an order of six for daytime (Figure 1i) in raw records showed lower performance ($R^2 = 0.29$; Figure 1h). RR models had lower AIC and BIC values than RMMs, indicating a better fit despite having lower parameter estimates. They also aligned with the raw data pattern. To our knowledge, no study has applied RR models to actual time series data, as previous studies have relied on standardised records based on group means (e.g., time, day).

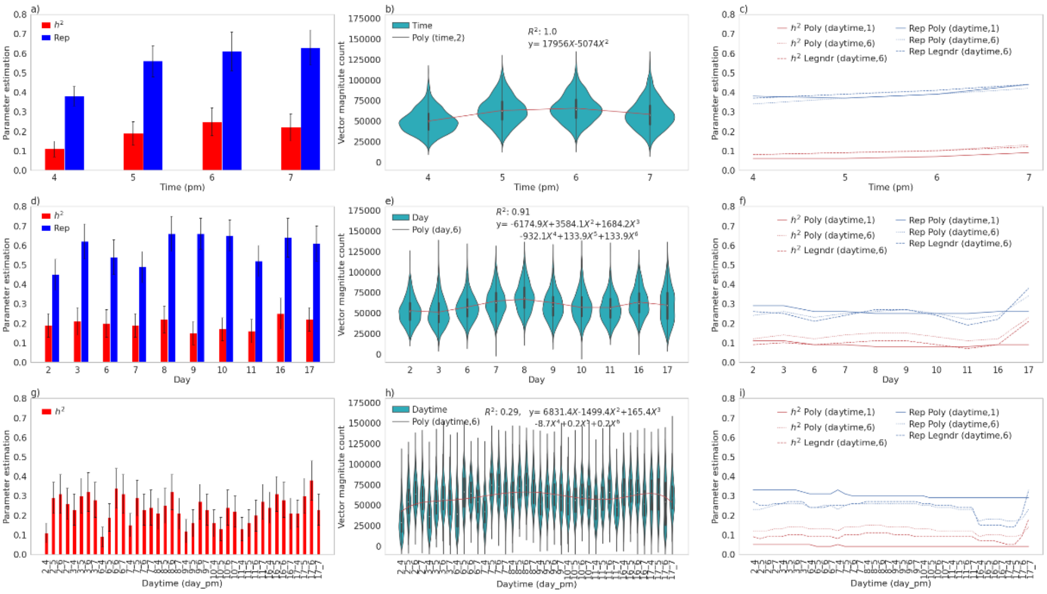

Figure 1. Plot showing parameter estimates (heritability-(h^2) and repeatability (Rep)) and data distribution across different times (a-c), days (d-f), and daytimes (g-i) obtained using various animal models. Note: Models included single estimates at intervals (time, day and daytime), linear random regression (first-order), Polynomial (poly) and Legendre (legendr) with a second order for the time, a sixth order for day and daytime.

Table 1. Genetic correlations across days (upper), and time points (lower diagonal) modelled using sixth-order and second-order polynomials, respectively

.

Day 3	Day 6	Day 7	Day 8	Day 9	Day 10	Day 11	Day 16	Day 17	Days
0.90	0.86	0.84	0.82	0.83	0.86	0.88	0.83	0.54	Day 2
	0.91	0.89	0.90	0.91	0.93	0.91	0.79	0.37	Day 3
		0.99	0.97	0.96	0.95	0.91	0.78	0.34	Day 6
			0.99	0.98	0.96	0.89	0.75	0.26	Day 7
				0.99	0.97	0.90	0.74	0.22	Day 8
					0.99	0.92	0.76	0.25	Day 9
						0.97	0.81	0.37	Day 10
							0.87	0.56	Day 11
								0.68	Day 16

5 PM	6 PM	7 PM	Times
0.90	0.84	0.74	4 PM
	0.97	0.73	5 PM
		0.86	6 PM

* Standard errors ranged from 0.03 to 0.04 for genetic correlations estimated between different times and from 0.02 to 0.04 between different days.

High genetic correlations (r_g) were found between times, and days, except for day 17, which had lower correlations with all other days (0.22–0.68; Table 1). There were also moderate to high r_g between different daytimes except for 78 daytime combinations with r_g lower than 0.6 (not shown). Almasi *et al.* (2023) also represented that there was a low intraclass correlation between measurements longer than one week. Overall, the result of this study indicate that there was no marginal difference in r_g across studied times and days. Therefore, considering the measurements across a broader range of time points and days might provide a more accurate view of actual h^2 and Rep estimated via the RR model compared to a single estimation of RMMs.

Previous studies on sheep activity have shown traits such as Daily Distance Travelled have moderate h^2 (0.36 ± 0.09) and Rep (0.51 ± 0.03) (Johnson *et al.* 2021). Almasi *et al.* (2023) reported that accelerometer-derived traits, such as grazing time, show moderate to high h^2 (0.44 ± 0.23) and Rep (0.70 ± 0.03) that can be useful for ranking animals for feeding activities in selective breeding programs (Almasi *et al.* 2023). Similarly, grazing behaviour traits in semi-extensively reared Boutsko sheep demonstrate significant h^2 and Rep for grazing and speed but low non-significant h^2 for distance (0.05 ± 0.06) (Vouraki *et al.* 2025). These findings highlight the value of wearable sensors for advancing genetic selection in sheep by providing continuous data that enables the development of traits for improved health and production.

CONCLUSION

This study showed moderate heritability and repeatability estimates for sheep activity, suggesting the potential of this novel trait for selection that may offer favourable correlated responses for health and production. Further work is required to determine the relationships between activity and health status, and between activity and economically important production traits. Although a weak pattern was observed in the results when considering RR models, our findings suggest that RMMs suffice for accurately estimating the genetic parameters in this dataset.

ACKNOWLEDGEMENTS

The authors thank Australian Wool Innovation and the Merino Lifetime Productivity (MLP) Project for use of the sheep and data in this study, and CSIRO Chiswick technical staff for conduct of the field work component.

REFERENCES

Almasi F., Stear M.J., Khansefid M., Nguyen H., Desai A., and Pryce J.E. (2023) *Front. Anim. Sci.* **4**: 1154797.

Brown D.J., Atkins K. and Huisman A.E. (2005) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **16**: 84.

Brito L.F., Oliveira H.R., McConn B.R., Schinckel A.P., Arrazola A., Marchant-Forde J.N. and Johnson J.S. (2020) *Front. Genet.* **11**: 793.

Gilmour A.R., Gogel B.J, Cullis B.R. and Thompson R. (2009) ASReml User Guide Release 3.0. VSN International Ltd, Hemel Hempsted, UK.

Johnson P., Cullen N., Hickey S., Knowler K., Bryson B., Hall M. and Pletnyakov P. (2021) *P.N.Z. J. Anim. Sci. Prod.* **81**: 68.

Hu S., Reverter A., Arablouei R., Bishop-Hurley G., McNally J., Alvarenga F. and Ingham A. (2024) *Animals* **14**: 301.

Marchesini G., Mottaran D., Contiero B., Schiavon E., Segato S., Garbin E., Tenti S. and Andrighetto I. (2018) *Vet. J.* **231**: 41.

Morris J.E., Cronin G.M. and Bush R.D. (2012) *Anim. Prod. Sci.* **52**: 665.

Ramsay A., Swan A. and Swain B. (2019) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **23**: 512.

Vouraki S., Papanikolopoulou V., Argyriadou A., Priskas S., Banos G., and Arsenos G (2025) *Applied Anim. Behav. Sci.* **282**: 106473.

Wang L., Arablouei R., Alvarenga F.A.P. and Bishop-Hurley G.J. (2023) *Comput. Electron. Agr.* **206**:107647.